

SEQUENCE LISTING

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 Kuettner, Klaus E.
 Schmid, Thomas M.
 Schumacher, Barbara L.
 Su, Jui-Lan

<120> SUPERFICIAL ZONE PROTEIN AND METHODS OF
 MAKING AND USING SAME

<130> 07083.0008U5

<150> 60/258,920

<151> 2000-12-29

<160> 11

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 1

Asp Glu Ala Gly Ser Gly

1

5

<210> 2

<211> 188

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 2

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Ser Val

1

5

10

15

Phe Val Ile Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly

20

25

30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr

35

40

45

FastSEQ 4.0

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
 50 55 60
 Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
 65 70 75 80
 Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
 85 90 95
 Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val Lys Asp Asn Lys Lys
 100 105 110
 Asn Arg Thr Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu
 115 120 125
 Ala Gly Ser Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp
 130 135 140
 Thr Ser Thr Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr
 145 150 155 160
 Thr Ala Lys Pro Ile Asn Pro Arg Pro Gln Ser Ser Pro Asn Ser Asp
 165 170 175
 Thr Ser Lys Glu Thr Ser Leu Thr Val Asn Lys Glu
 180 185

<210> 3

<211> 538

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 3

Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro Glu Leu Ser
 1 5 10 15
 Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys Glu Pro Gly
 20 25 30
 Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu Met Thr Thr
 35 40 45
 Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr Thr Pro Glu
 50 55 60
 Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala Thr Thr Thr
 65 70 75 80
 Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr Gln Val Thr
 85 90 95
 Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr Thr Leu Lys
 100 105 110
 Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys Thr Ile Thr Thr
 115 120 125
 Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys Pro Lys Asp Arg
 130 135 140
 Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln Lys Pro Thr Lys
 145 150 155 160
 Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys Thr Met Pro Arg
 165 170 175
 Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met Thr Ser Thr
 180 185 190

1003694.2304

Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala Met Leu Gln
195 200 205
Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu Val Glu Val
210 215 220
Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu Thr Pro His
225 230 235 240
Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr Pro Asp Met
245 250 255
Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile Asn Pro Met
260 265 270
Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val Asp Gly Leu
275 280 285
Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg Gly His Tyr Phe
290 295 300
Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala Arg Arg Ile Thr
305 310 315 320
Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val Phe Thr Arg Cys
325 330 335
Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser Gln Tyr Trp Arg
340 345 350
Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys Pro Ile Phe Lys
355 360 365
Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala Leu Ser Thr Ala
370 375 380
Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe Lys Arg Gly Gly
385 390 395 400
Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val Gln Lys Cys Pro
405 410 415
Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly Glu Met Thr Gln
420 425 430
Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro Ser Gln Thr His
435 440 445
Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala Tyr Gln Asp Lys
450 455 460
Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu Trp Arg Gly Leu
465 470 475 480
Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro Asn Ile Arg Lys Pro
485 490 495
Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys Asp Gln Tyr Tyr Asn Ile
500 505 510
Asp Val Pro Ser Arg Thr Ala Arg Ala Ile Thr Thr Arg Ser Gly Gln
515 520 525
Thr Leu Ser Lys Val Trp Tyr Asn Cys Pro
530 535

<210> 4

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

FOI 201-46988007

<221> VARIANT

<222> 2

<223> Xaa is any amino acid except Pro

<221> VARIANT

<222> 3

<223> Xaa is either Thr or Ser

<400> 4

Asn Xaa Xaa

1

<210> 5

<211> 488

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 5

atgcatgaaa cattccatta ctgtgttctg tggtgtttct gatcacaatt tatccaaatt	60
atcagcgtga ggagagtggg agggatttag gatccactga acgtgttaaa cgtcacatac	120
tgggtgtgcc tgtttaagga gctgactcgg gcttccgtaa ggcgcgcttg atcctcggag	180
gggggggtgg acgcgcgcca agtagaatat acagtgtgtc cgttagaggt ttctgtgcag	240
aagtaaaaga taacaagaag aacagaacta aaaagaaacc taccaccaaa ccaccagttg	300
tagatgaagc tggaagtgga ttggacaatg gtgacttcaa ggtcacaact cctgacacgt	360
ctaccacca acacaataaa gtcagcacat ctccaagat cacaacagca aaaccaataa	420
atcccagacc ccagtcctca cctaattctg atacatctaa agagacgtct ttgacagtga	480
ataaagag	488

<210> 6

<211> 1620

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 6

cctaccacta tccacaaaag cctgatgaa tcaactcctg agctttctgc agaaccaca	60
ccaaaagctc ttgaaaacag tccaaggaa cctgggtgtac ctacaactaa gactcctgca	120
gcgactaaac ctgaaatgac tacaacagct aaagacaaga caacagaaag agacttacgt	180
actacacctg aaactacaac tgctgcacct aagatgacaa aagagacagc aactacaaca	240
gaaaaaacta ccgaatccaa aataacagct acaaccacac aagtaacatc taccacaact	300
caagatacca caccattcaa aattactact cttaaaacaa ctactcttgc acccaaagta	360
actacaacaa aaaagacaat tactaccact gagattatga acaaacctga agaaacagct	420
aaacccaaaag acagagctac taattctaaa gcgacaactc ctaaacctca aaagccaacc	480

```
<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence; note =
synthetic construct

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<400> 7
atggcatgga aaacaatttc catt
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```
<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence; note =
synthetic construct

```
<400> 8
ctaaggacag ttgtaccaga cttt
```

```
<210> 9
<211> 4
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence; note =
synthetic construct

Variable	Mean	SD	Min	Max
Age	34.2	10.5	20	55
Gender	1.2	0.4	1	2
Marital status	1.5	0.5	1	3
Education	12.5	1.5	9	16
Income	15.2	3.5	10	25
Occupation	1.8	0.8	1	4
Health status	1.5	0.5	1	3
Stress level	2.5	1.0	1	4
Life satisfaction	3.5	1.0	1	5
Resilience	2.8	0.8	1	4
Optimism	3.2	0.8	1	4
Self-efficacy	3.0	0.8	1	4
Emotional stability	3.8	0.8	1	5
Prosocial behavior	3.5	0.8	1	5
Empathy	3.2	0.8	1	5
Altruism	3.0	0.8	1	5
Compassion	3.5	0.8	1	5
Kindness	3.2	0.8	1	5
Generosity	3.0	0.8	1	5
Helpfulness	3.5	0.8	1	5
Cooperativeness	3.2	0.8	1	5
Teamwork	3.0	0.8	1	5
Leadership	3.5	0.8	1	5
Communication	3.2	0.8	1	5
Conflict resolution	3.0	0.8	1	5
Problem solving	3.5	0.8	1	5
Decision making	3.2	0.8	1	5
Goal setting	3.0	0.8	1	5
Time management	3.5	0.8	1	5
Organization	3.2	0.8	1	5
Productivity	3.0	0.8	1	5
Efficiency	3.5	0.8	1	5
Quality of work	3.2	0.8	1	5
Job satisfaction	3.0	0.8	1	5
Work-life balance	3.5	0.8	1	5
Stress management	3.2	0.8	1	5
Emotional regulation	3.0	0.8	1	5
Self-awareness	3.5	0.8	1	5
Empathy	3.2	0.8	1	5
Altruism	3.0	0.8	1	5
Compassion	3.5	0.8	1	5
Kindness	3.2	0.8	1	5
Generosity	3.0	0.8	1	5
Helpfulness	3.5	0.8	1	5
Cooperativeness	3.2	0.8	1	5
Teamwork	3.0	0.8	1	5
Leadership	3.5	0.8	1	5
Communication	3.2	0.8	1	5
Conflict resolution	3.0	0.8	1	5
Problem solving	3.5	0.8	1	5
Decision making	3.2	0.8	1	5
Goal setting	3.0	0.8	1	5
Time management	3.5	0.8	1	5
Organization	3.2	0.8	1	5
Productivity	3.0	0.8	1	5
Efficiency	3.5	0.8	1	5
Quality of work	3.2	0.8	1	5
Job satisfaction	3.0	0.8	1	5
Work-life balance	3.5	0.8	1	5
Stress management	3.2	0.8	1	5
Emotional regulation	3.0	0.8	1	5
Self-awareness	3.5	0.8	1	5

<400> 9

Phe Ala Cys Glu

1

<210> 10

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 10

Val Lys Asp Asn Lys Lys Asn Arg

1

5

<210> 11

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<221> VARIANT

<222> 8

<223> Xaa is either Thr or Pro

<400> 11

Lys Glu Pro Ala Pro Thr Thr Xaa

1 5

2

5

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